

Fig. 1

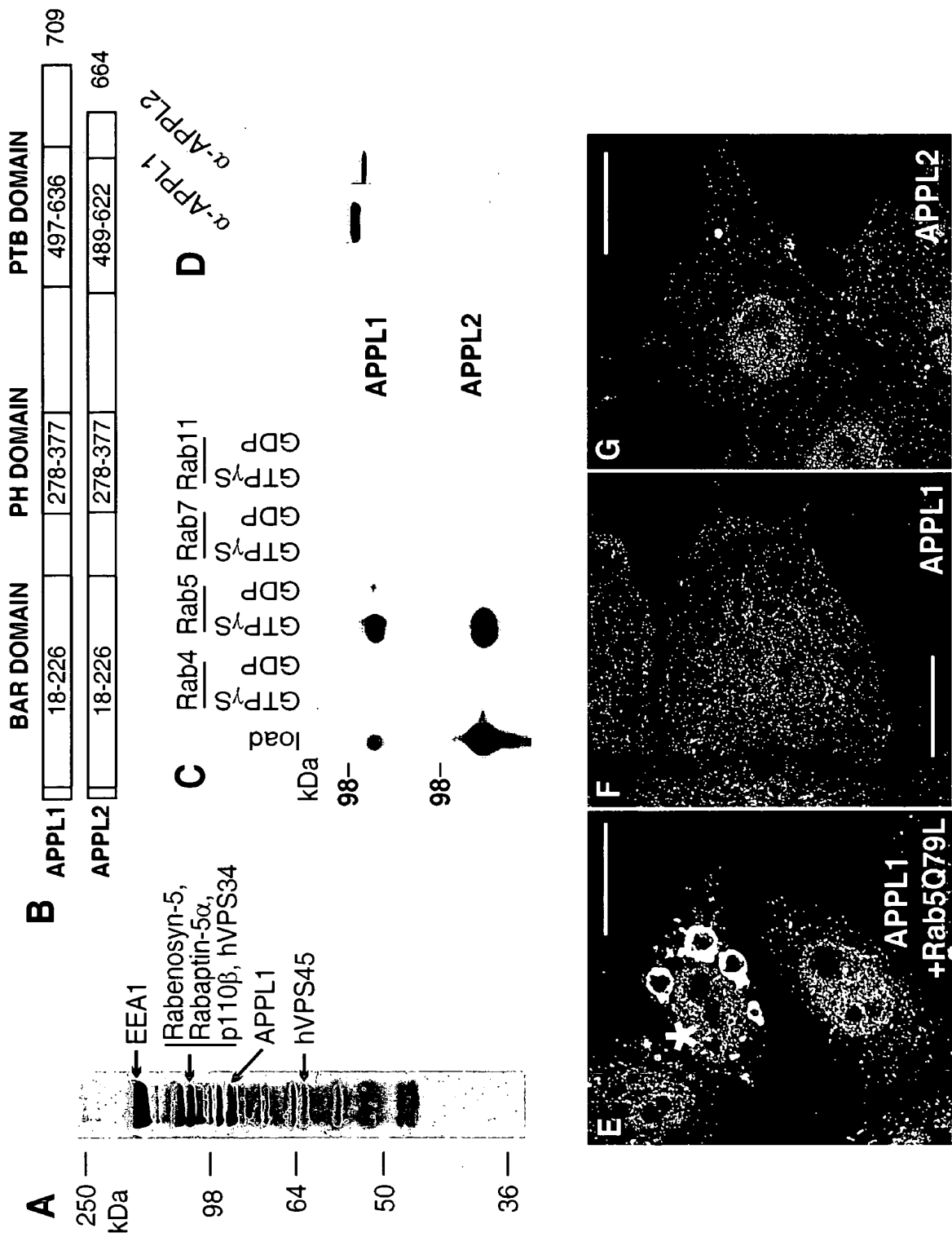


Fig. 2

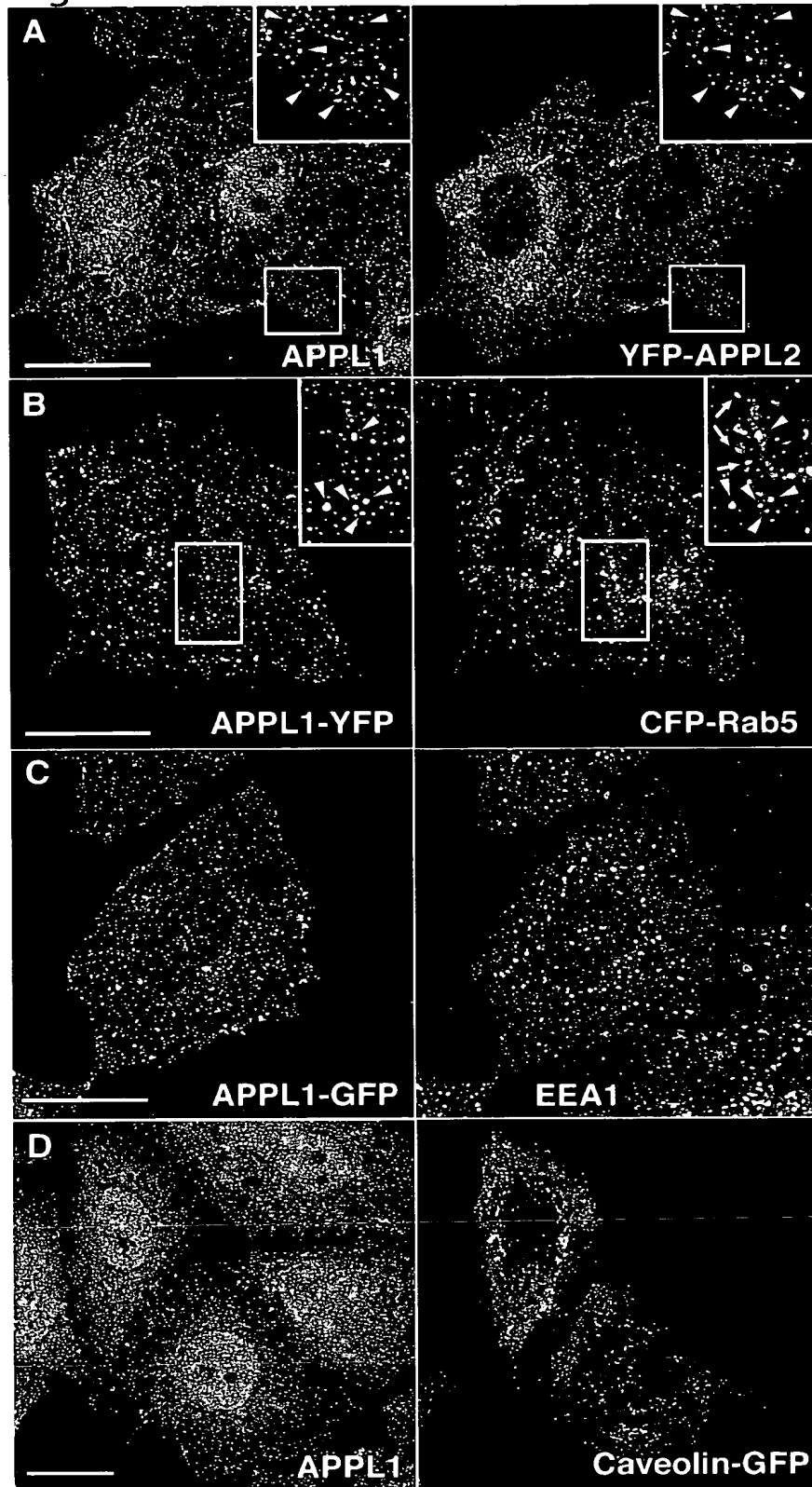


Fig. 3

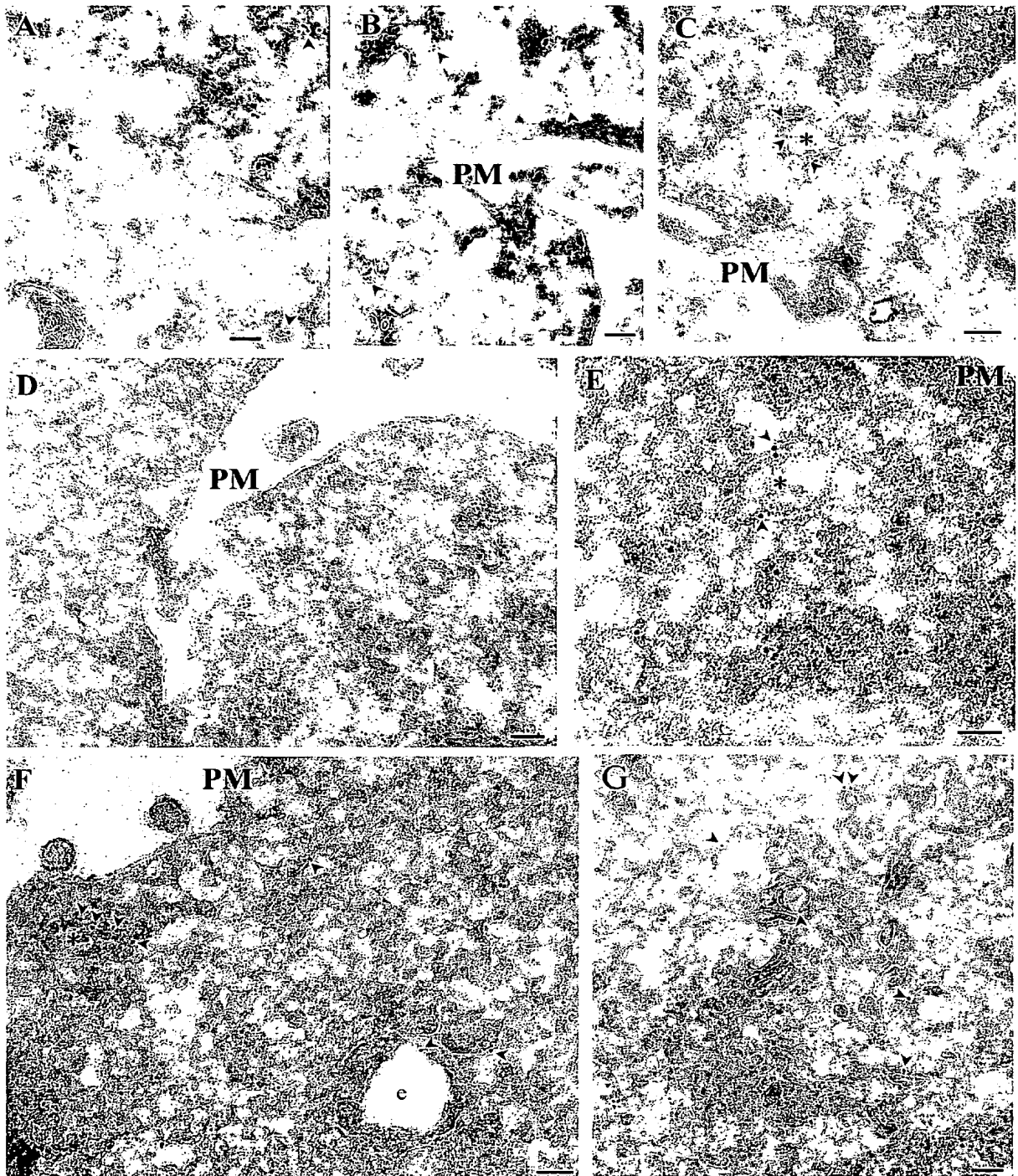


Fig.4

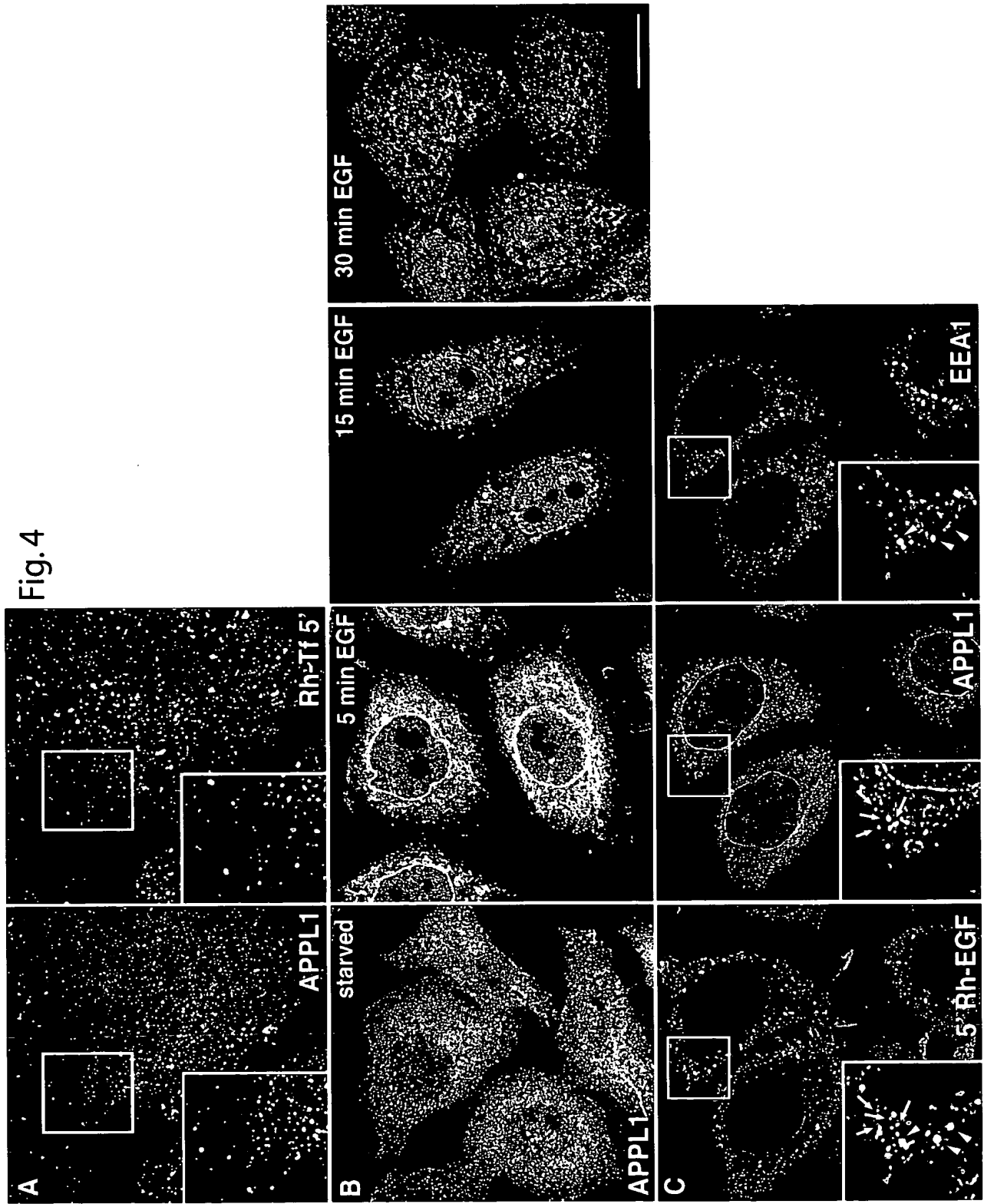


Fig. 5

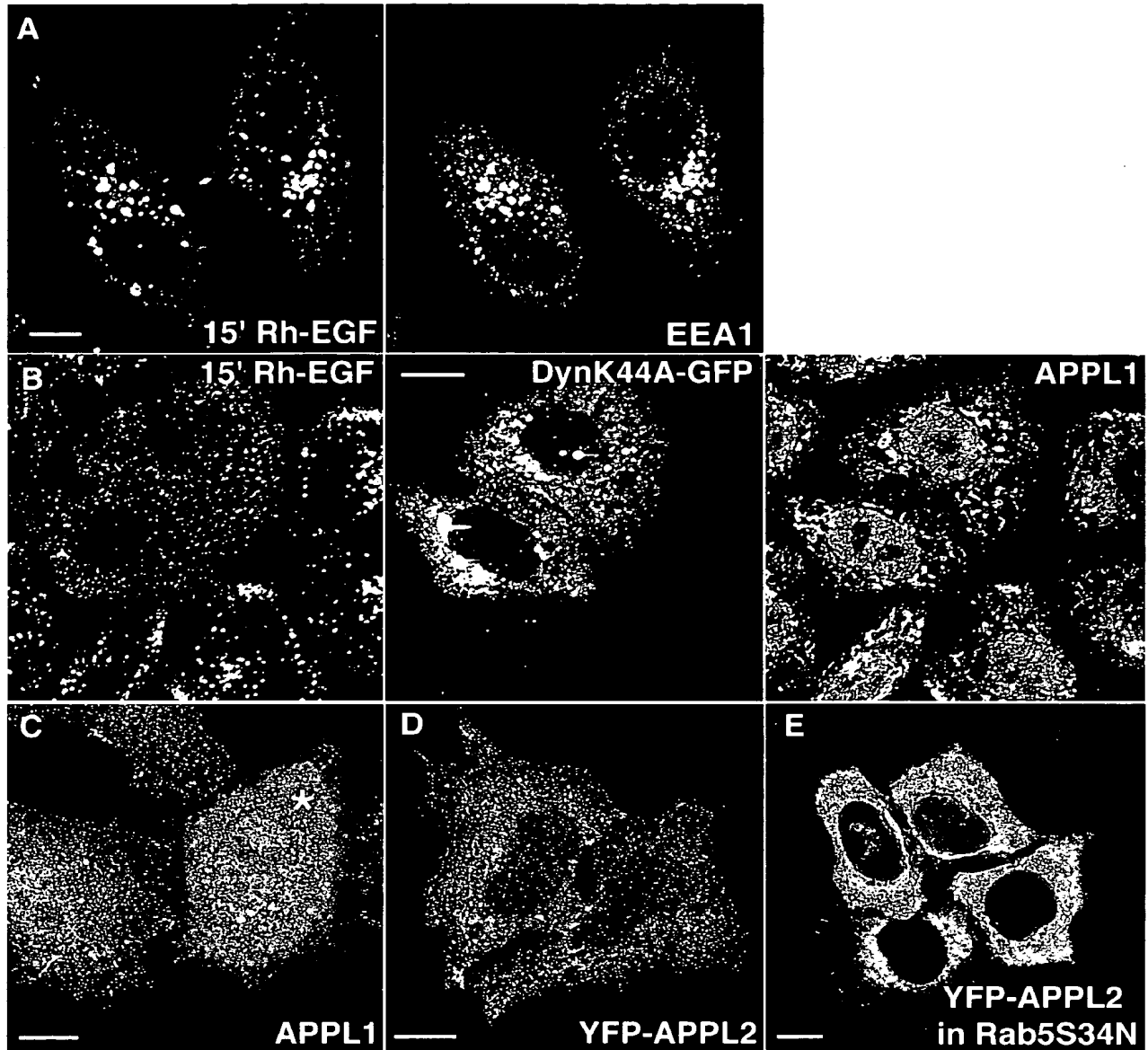
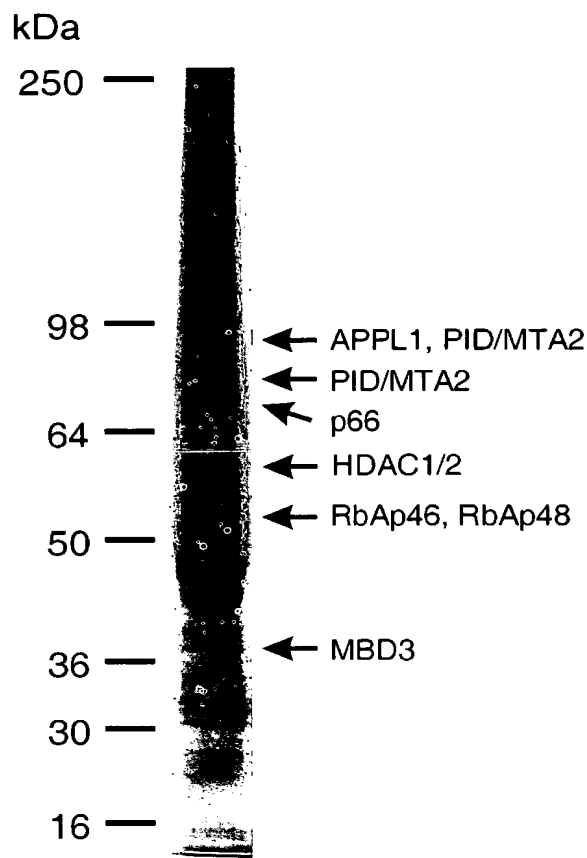
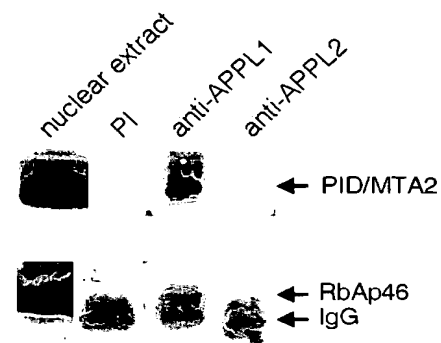


Fig. 6.

**A**



**B**



**C**

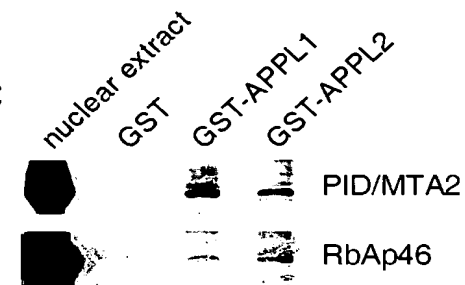


Fig. 7

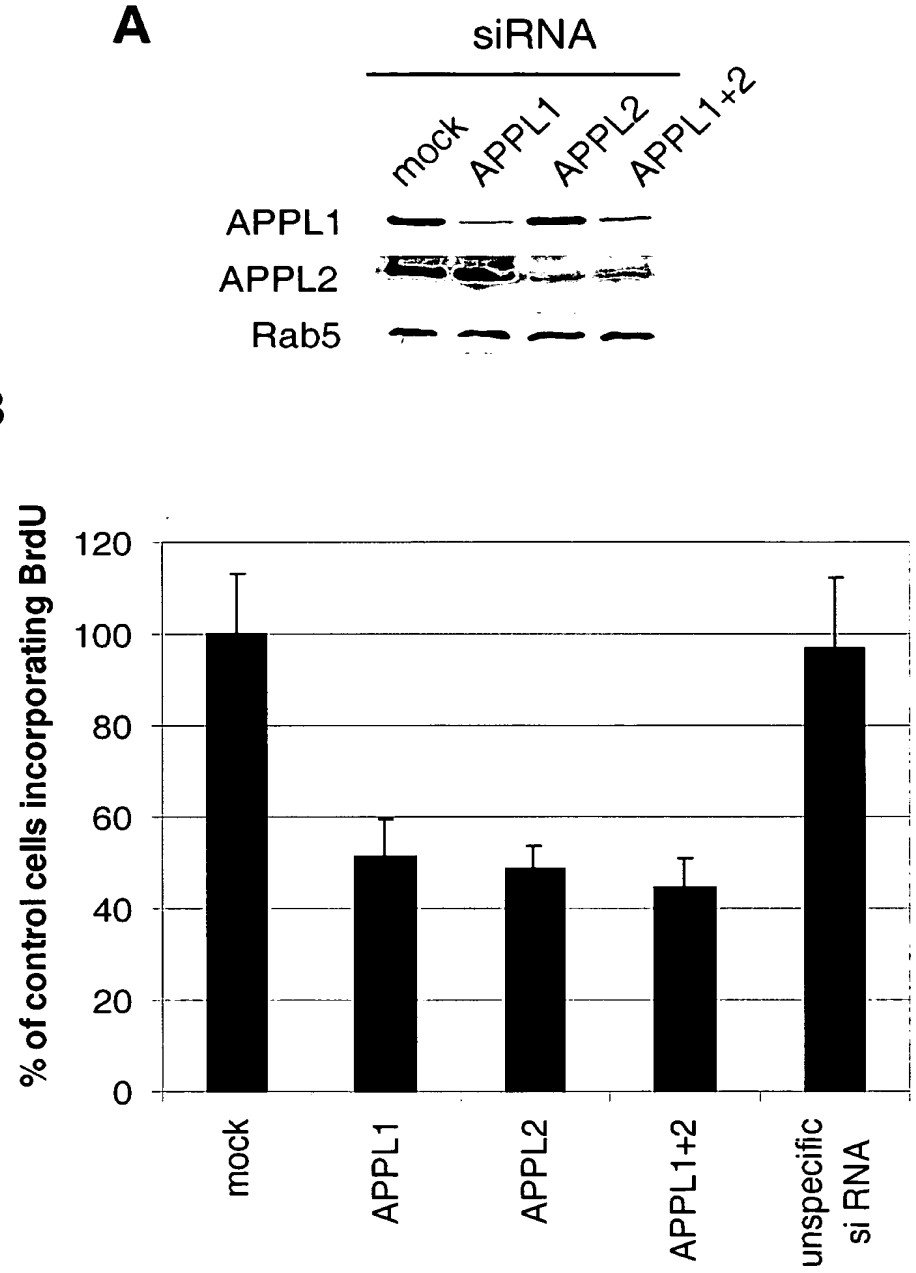


Fig. 7

**C**

	BAR DOMAIN	PH DOMAIN	PTB DOMAIN	Rab5 binding	localization	% of BrdU incorporation
APPL1	18-226	278-377	497-636	+	V	100
			Δ532-709	+	V	100
		Δ429-709		+	V, C	100
	Δ320-709			-	C, N	0 (cell death)
				-	C	0
			Δ1-272	-	C, N	30-40
			Δ1-491	-	C, N	20
		273-384		-	C, N	30-40
			273-531	-	C, N	30-40



Fig.8

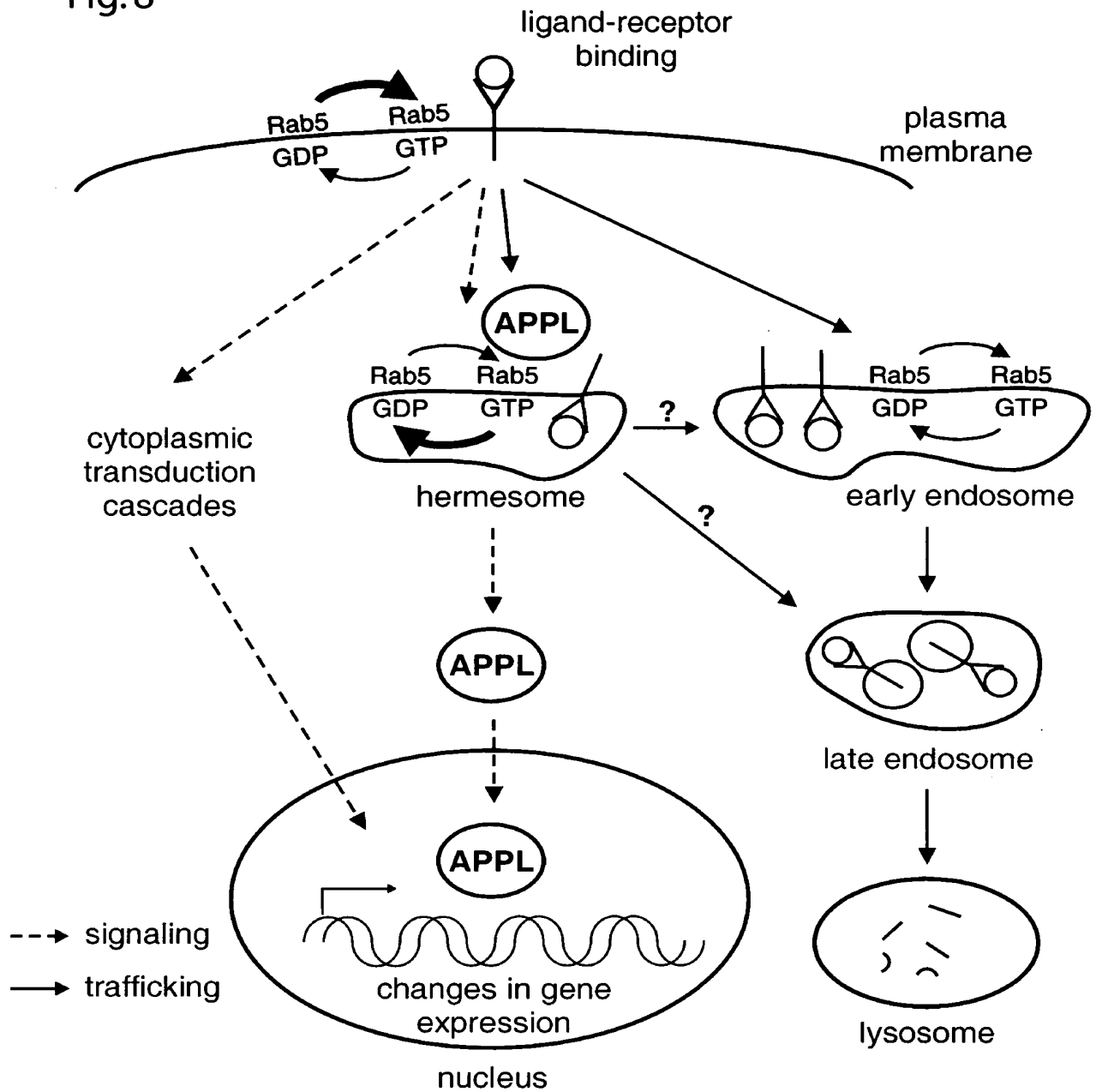


Fig. 9

HsArfaptin2	ARGIAGEPDIIVKMGINIVKCTKQILLSERPGRGSRVDTLELELQIELARETKKVESVQLGRALTAHLYSLIQTHALGDAFADLSQSPPELQEEFG 185
MmArfaptin2	ARGIAGEPDIIVKMGINIVKCTKQILLSERPGRGSRVDTLELELQIELARETKKVESVQLGRALTAHLYSLIQTHALGDAFADLSQSPPELQEEFG
HsArfaptin1A	IKNPAMEKDELVRMSLNIVKCTPQILSEKLGSRGVDTLELEAQIDILRDNKKKVENILKLAQTISTQLFQMVHTQRQLGDAFADLSLSLELHEEFG
XlArfaptin1	PRSTAVEKDELVRMSLNIVKCTPQILSEKLGSRGVDTLELESQIEILRDNKKKVENILKLAQTISTQLFQMVHTQRQLGDAFADLSLSLELHEEFG
DmArfaptin	IIRTSASKIDSLKNWSISIVKCTPQIMLEKLGSRGVDTSELEAQIEQLRETQRKKLSTLRLLTRAFSSHFQHVVVVTHALADSEADLAQKNPELQKEFT
CeArfaptinA	DTAQVAAGVDSFKKMTIGLFFKNSKQQLLEHMEKIDKRVDPFEAQCEVLDIHRMGGLVWAAAKNPFSHVLTQMAEAEKKLSSEFYQLSMFEQIKAQCT
HsAPPL-bar	-----QTRSLGVFEEDATAISNYMNQIYQAMHRIYDAQNELSAATH-----LTSKLLKEVEKQRPFLGGDDVMSSTLQQFSKVIDELSS--- 99
MmAPPL-bar	-----QTRSLGVFEEDATAISNYMNQIYQAMHRIYDAQNELSAATH-----LTSKLLKEVEKQRPFLGGDDVMSSTLQQFSKVIDELSS---
XlDip13A	-----QTRSLGVFEEDATAISSYNNKLIFHAMRRIYDAQNELSAATH-----LTSKLLKEVEKQRPFLGGDDVMTSTLQQFSKVIDELSS---
HsDip13B	-----QTRSLSVFEEDAGTLTDYTNQLQAMQRYGAQNMCLATQQ-----LSKQLLAYEKQNFALCKGDEEVI STLHYFSKVVDLNLNLT
MmDip13B	-----QARSLSVFEEDAGTLTDYTNQLQAMQRYGAQNMCLATQQ-----LSRQLLAYEKQNFALCKGDEEVI STLHYFSKVMDLNLNLT
HsArfaptin2	YNADTOKLICKKNGETLLGAVNFFVSSSNTLVTYKMEDETLMTVKQ-YEAAAEYDAYRTDLEELSLGSRDAGTRGRLESAQATFOAHRDKYEKLRGDVAI 285
MmArfaptin2	YNADTOKLICKKNGETLLGAVNFFVSSSNTLVTYKMEDETLMTVKQ-YEAAAEYDAYRTDLEELSLGSRDAGTRGRLESAQATFOTHRDKYEKLRGDVAI
HsArfaptin1A	YNADTOKLICKKNGETLLGAINFFIASVNTLVNKHIEDTLMTVKQ-YESAPTEYDAYRTDLEELNLGSRDANTELPKIEQSQHLFOAHKEKYDKVRNDVSV
XlArfaptin1	YNADTOKLICKKNGETLLGAMNFFISGVNTLVNKHIEDTLITVKQ-YEASPTHEYDAYRTDLEELNLGSRDAITMPKIEQSQQLFQSHKEKYDKVRNDVSV
DmArfaptin	CNSETORNITKNGGELLNAINLNFPISSVNTLVNKHIEDTLITIRQ-YETAPTEHFDAYRVDLEN--TKPELTPSAVALLEETQRSVAQHKEQYEKLRSDVAV
CeArfaptinA	MTSETMRGVGEQAASLDACLRYEILSSMETVYNQHTDTLHTIYN-TESAPTEHYDVEDNDLSAATNPQOQLTKNLPVGATEKCEKKAKEYEKLKADVAI
HsArfaptin2	-----CHAVLSTQLADAMNFPITQPK-----ERDLKE-ILTLKEVFQIASNDHDAAINRYSR--LSKKRENDKVKYEVTEDEVYTSRKKQHQTMMHYFCA 186
MmAPPL-bar	-----CHAVLSTQLADAMNFPISQPK-----ERDLKE-ILTLKEVFQIASNDHDAAINRYSR--LSKKRENDKVKYEVTEDEVYTSRKKQHQTMMHYFCA
XlDip13A	-----CQAILSTQLADAMNFSIGQPK-----ERDLKE-ILTLKEVFQIASNDHDAIVAINRYSR--LSKPRENEKTKTEATEDVYTARKQHQTMMHYFCA
HsDip13B	-----ELAKQLADTWLPPIIQPR-----EKDLTE-VSTLKDIFGLIASNEHDLISMAKYSR--LPKKKENEKVKTEVGKEVAARRKQHLSSLSQYYCA
MmDip13B	-----ELAKQLADTWLPVPIQPR-----EKDLTE-VSTLKDIFGLIASSEHDLISMAKYSR--LPKKKENEKAKTEIVKEVAARRKQHLSSLSQYYCA

Fig. 9 (continued)

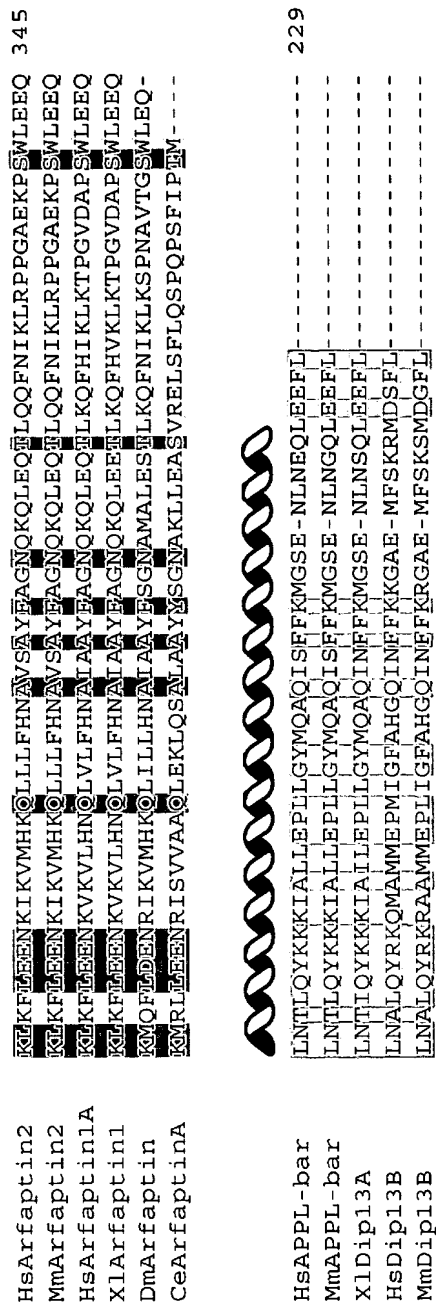
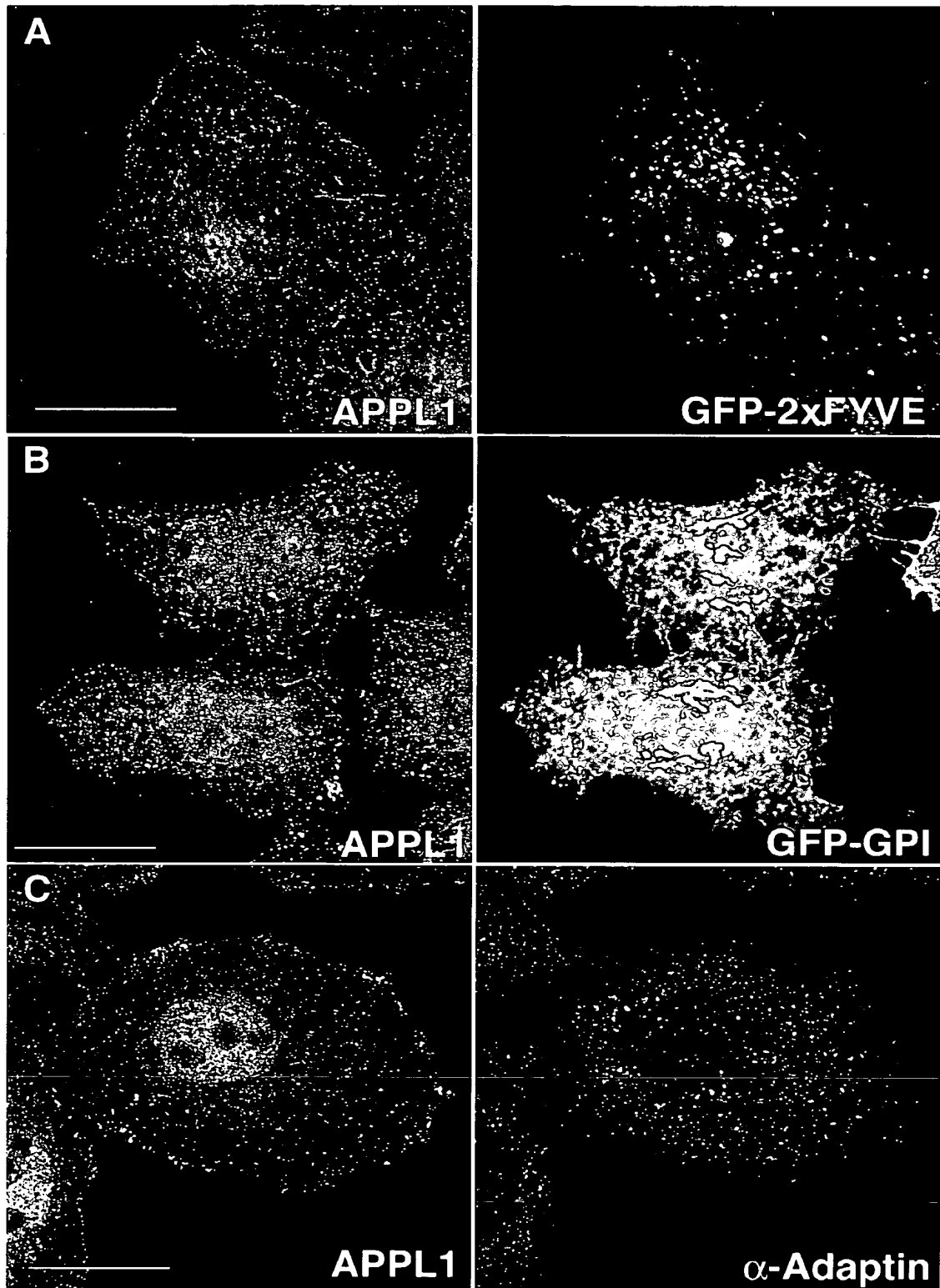


Fig. 10



**This Page is Inserted by IFW Indexing and Scanning  
Operations and is not part of the Official Record**

**BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☒ FADED TEXT OR DRAWING
- ☒ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☒ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☒ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: \_\_\_\_\_

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.**